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AC013439 Homo sapi
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AX188131 Sequence
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AX083764 Homo sapi
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AX339606 Sequence
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 167891)

Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Nguyen,C., Cotton,M., Hawkins,M. and Spalding,L.
The sequence of Homo sapiens BAC clone RP11-270G18
Unpublished
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                                              AF226614
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Waterston, R.H.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
McP. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The clone sequenced to the left is AC068833; the clone sequenced to the right is RP11-88L20, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-270G18; actual end is at base position 167891 of RP11-270G18.

Location/Qualifiers
1. 167891
                                                                                                                                                                                                                                                Direct Submission`
Submitted (07-NOV-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 10, 2001 this sequence version replaced gi:12280930.
                                                                                                                                                    Washington
Missouri 63108, USA
Submitted (11-NOV-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (1989) (1980) (1980) (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    all regions were double stranded, sequenced with an alternate chemistry. or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                  Direct Submission
Submitted (09-AUG-2001) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
5 (bases 1 to 167891)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                        NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://bacpac.med.buffalo.edu)
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                                                                                                   Waterston, R.
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                                                                                                                                                                                                                                                     TITLE
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(NID:g1630415) mk22h02.r1"
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                                                                                                                                                                                                                                                                                                                                                          EST BF693237 (NID:911978645)"
                                                                                                                                                                                                                                       AV727426 (NID:910836847)"
                                                                                                                                                                                                                                                                                                EST AU124827 (NID:910949543)"
                                                                                                                                                                                                                                                                                                                                                                                                                   BG035852 (NID:g12430401)"
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                                                                                                                                                                                                                                                                                                                                                                                      EST AU132620 (NID:910993159)"
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                                                                                                                                                                                                                                                                    BE242721 (NID:99094452)"
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b EST BF693237 (NID:911978645) c EST AA087204 (NID:91630415) c EST AV727426 (NID:910836847) c EST AU124827 (NID:910949543) c EST BE247703 (NID:99099550)" c EST BE247703 (NID:910204900) c EST BE891195 (NID:910350282) c EST BG035852 (NID:912430401)	similar to EST AL543591 (NID:g12876070)" 12500 similar to EST AW121877 (NID:g6097251)" 12500 similar to EST BF334128 (NID:g11304876)" 12500 similar to EST A1556441 (NID:g4488804)" 12826 similar to EST BE242721 (NID:g9094452)" similar to EST BE242721 (NID:g9094452)" 13277 similar to EST BE931679 (NID:g12349003)" 1.58, Score 3113, DB 9; Length 167891; s. 88; Pred. No. 0; Nismatches 115; Indels 442; Gaps 4;	ttcactttaaatcggtggtgataaatgaggctgtaagcttgtttttgttctgggtatt 3775
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g	127128		127069
Ωy	6311		6310
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Q O	126/08	GAAACIGITITTATCITGIGATACAAAACAGTICATTAGITTATTG	26
ò a	6516	agatattaatttccaggcaagacagctttattgtttgggctttagaactctagcagtaat 	6575
ΟY	6576	aaagtttccttacactttaaccataaccatttattaggtcattt	63
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qq	126468	- 55	126409
οy	6756	ttctttttgtctgatgactgtaaaaatcatttattgaggccactaataacccaatattta	6815
ΩĐ	126408	TTTGTCTGATGACTGTAAAAATCATTTATTGAGGCCACTAATAACCCAATATT	126349
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Οy	6876	caggctaaaatgtatattttgcatatgtcaacagatttttatctgtgatttgaaatgtat	
QQ	126288	SCTAAAATGTATTTTGCATATGTCAACAGATTTTTATCTGTGTTTGAAATG	126229
Qγ	9869	gcctgtaaactaaaatctaatctttaaaaaaatatttatt	6995
qq	126228	CCTGTAAACTAAAATCTTTAAAAAATATTTTATTATAGGTCTTTGGTCCTTT	126169
ογ	669	atttaactgtgacacagttgctgcaagaaaatgtaattgaatctgaaagaggcattataa	7055
Ор	126168	raactgtgacacagttgctgcaagaaaatgtaattgaatctgaaagagg	126109
οy	7056	atggtgtacagaactccatgaactatcttcttgatcttctgcatttcatcatggtcatcc	7115

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NOTE: This record contains 78 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preserved.

781 880: gap of 100 bp 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10364 10463: gap of 100 bp 11258 11357; gap of 100 bp 11258 11357; contig of 794 bp in length 11258 11357; gap of 100 bp 11358 12109: contig of 752 bp in length 1210 12209; gap of 100 bp 12110 122973; contig of 764 bp in length 12974 13033; gap of 100 bp 13074 13916; gap of 100 bp 13917 14688; contig of 772 bp in length 13817 14688; contig of 772 bp in length 14789 14789; gap of 100 bp 14789 1488; gap of 100 bp 16560 15659; gap of 100 bp 16561 14789; gap of 100 bp 16560 15659; gap of 100 bp 16560 16442; contig of 783 bp in length 15660 16442; contig of 783 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the record is updated, the accession number will
be preserved.
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10069; contig of 774 bp in length
69; gap of 100 bp
19933: contig of 764 bp in length
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22525: contig of 763 bp in length
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18195: contig of 778 bp
                                                                                                                                                                                                                                                                                                        Center project Information
Center project name: L10434
Center clone name: 383_0_1
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Shaess I to 67729)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Boguslavkiy, L., Bodwin, J., Barna, N., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Gland-Fierre, N., Grand, G., Hagos, B., Haaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, R., Meheeters, R., Meldrim, J., Meneus, L., Mihowa, T., Miranda, C., Mlenga, V., Morrow, J., Wurphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollyer, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollyer, Y., Raymond, C., Riley, R., Ropov, P., Rothman, D., Stange, Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Volny, G., Zahnon, J., Zimmer, A. and Zody, M., X., Wyman, D., Ye, W.J., Pirrel, Shimission, R., Why, K., Wyman, D., Ye, W., Shimer, Shimission, R., Warter, Sh
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Homo sapiens chromosome 2 clone RP11-38301 map 2, LOW-PASS SEQUENCE
SAMPLING.
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1 (bases 1 to 67729)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 2, clone RP11-38301
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Db 126108 ATGGTGTACAGAACTCCATGAACTATCTTCTTGATCTTCTGCATTTCATGGTCATCC 126049
                                                                                                                                                                                                                                                              Db 125928 GCGCTCCTGATGCAAAAGAAGTTAGGAAGGAAAATCAAGCAAATACATCTGTTTTGAG 125869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DD 126048 TGGCTCCAAATCCTGAAGCTTTTGGCTTGCTCGTATTGATTTCAGTCTCCTTTGTGGCAA 125989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 125808 CTGCAGAATTCCAATAAATGGCTGGGTGTTTTGCTCTGTTTTACCACACGCTGTGCCTTG 125749
                                                                                                                                                                                                                                                                                                                                                                                                                                              geggteetgatgeaaaagaagttaggaaggaaaateaageaaatacatetgttgtttgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctgcagaattccaataaatggctggtgttttgctctgttttaccacagctgtgccttg
                                                                                            tggctccaaatcctgaagcttttggcttgctcgtattgatttcagtctcctttgtgggcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7416 agaactaaaagctgtttaggaaacctaagtcagcagaaattaactgattaatttccctta
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RESULT 2 AC073035/c DEFINITION

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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE AUTHORS TITLE JOURNAL

REFERENCE

REFERENCE AUTHORS

in length

TITLE JOURNAL

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13.248: contig of 782 bp in length 31.248: contig of 782 bp in length 32.25: gap of 100 bp 32.25: gap of 100 bp 32.25: gap of 100 bp 33.05: contig of 773 bp in length 33.078: contig of 787 bp in length 33.078: contig of 787 bp in length 33.078: contig of 780 bp in length 33.078: contig of 780 bp in length 35.23: contig of 780 bp in length 35.23: gap of 100 bp in length 35.23: gap of 100 bp in length 35.23: contig of 762 bp in length 37.06: contig of 762 bp in length 37.06: contig of 762 bp in length 39.082: contig of 770 bp in length 100.1: gap of 100 bp in length 100.2: gap of 100 bp in length 100.2: gap of 100 bp in length 1256: contig of 770 bp in length 1256: gap of 100 bp in length 1250: contig of 770 bp in length 1250: contig 
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53853: contig of 7
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34725: contig of 34825: gap of 1
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23395: contig c
23495: gap of
24279: contig o
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26024: contig o
26124: gap of
26902: contig o
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46016: cont
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47730: cont
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25149: con
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31248: con
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32978; cont
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39082: cont
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45170: cont
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                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                         Length 67729;
            19 54818; gap of 100 bp 15573; contig of 755 bp in length 14 55673; contig of 755 bp in length 14 55457; contig of 784 bp in length 58 5657; gap of 100 bp 15420; contig of 783 bp in length 15420; gap of 100 bp 100 bp 15818; contig of 778 bp in length 158198; contig of 778 bp in length 159 58298; gap of 100 bp 100 bp
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                                                                                                                                                                                                                                                                                                         Score 684.8; DB 2;
Pred. No. 1.2e-124;
0; Mismatches 7;
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59946: contlg of 764 bp in
60046: gap of 100 bp
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RESULT

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12210 12203: 9ap of 100 bp 12373: contig of 764 bp in length 12374 13073: 9ap of 100 bp 13074 13073: 9ap of 100 bp 13074 130816: contig of 743 bp in length 13817 13916: 9ap of 100 bp 14789 14589: contig of 772 bp in length 14689 14589: aap of 100 bp 15559: contig of 771 bp in length 15560 15559: gap of 100 bp 15643 15447; gap of 100 bp 15543 17317: contig of 775 bp in length 16543 17317: contig of 775 bp in length 16543 18195: contig of 775 bp in length 16181 18195: contig of 774 bp in length 18196 18295: gap of 100 bp 17818 18195: contig of 774 bp in length 18296 19069: contig of 774 bp in length
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                                                                                                                                                                                                                                                                                                               to of 100 bp.

contig of 767 bp in length
ap of 100 bp.

contig of 794 bp in length
ap of 100 bp.
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: contig of 764 bp in length

lap of 100 bp

: contig of 787 bp in length

lap of 100 bp

: contig of 742 bp in length
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                             100 bp
f 790 bp in length
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f 768 bp in length
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25149: con
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     ACC73035 67729 bp DNA linear HTG 08-JUN-2000
Homo sapiens chromosome 2 clone RP11-38301 map 2, LOW-PASS SEQUENCE
SAMPLING.
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 67729)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-JUN-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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Homo sapiens chromosome 2, clone RP11-38301
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                                                                                                                                        AC073035.1 GI:8347978
HTG; HTGS_PHASE0.
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                                                                                                                                                                                                                               Homo sapiens
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KEYWORDS
SOURCE
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41697: contig of 760 bp in length
42569: contig of 763 bp in length
560: gap of 100 bp
43434: contig of 774 bp in length
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larity 97.5%; Pred. No. 2.2e-118;
Conservative 0; Mismatches 15;
   ap of 100 bp is contig of 762 bp in p of 100 bp is contig of 766 bp in
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36584: gap of
37346: contig of
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.u: gap of 46858:
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s: gap of
56457:
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gap of
57320:
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58198:
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.: gap of
59082:
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38212: cont
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2222)
Donovan, A., Brownlie, A., Zhou, Y., Shepard, J., Pratt, S.J., Moynihan, J., Paw, B.H., Drejer, A., Barut, B., Zapata, A., Law, T.C., Brugnara, C., Lux, S.E., Pinkus, S., Pinkus, J. L., Kingsley, P.D., Palis, J., Fleming, M.D., Andrews, N.C. and Zon, L.I.
Positional cloning of zebrafish ferroportini identifies a conserved
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Donovan, A., Brownlle, A., Shepard, J., Pratt, S.J., Paw, B.H., Barut, B.
and Zon, L.I.
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Submitted (20-JAN-2000) Hematology/Oncology, Children's Hospital,
300 Longwood Ave., Boston, MA 02115, USA
Location/Qualifiers
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gttgcccaggctgaagtgcagtggcgcgatcttggctcactgcaagctctgcctcctggg
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Homo saplens ferroportinl (FPNI) mRNA, complete cds.
AF226614
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305. 2020
/gene="FPN1"
/note="transporter; iron exporter"
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/chromosome="2"
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                                                                                                                                          1 (bases 1 to 2824)
Schlegel.R., DeedS,J., Berger,A. and Zhao,X.
Genes, compositions, Kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
Patent: WO 014246-A 400B 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
                                                                                                                        Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                      tch 8.6%; Score 647.6; DB 6; 31 Similarity 91.5%; Pred. No. 2.9e-117; 686; Conservative 0; Mismatches 64;
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4008 from Patent WO0142467.
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/db_xref="taxon:9606"
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1774 CATTATAAATGGTGTACAGAACTCCATGAA 1803
                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Conservative 0; Mismatches 64;
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1 (bases 1 to 3081)
Bandman,O., Hillman,J.L., Tang,Y.T., Lal,P., Yue,H., Baughn,M.R., Extracellular matrix and ablasion-associated proteins
Patent: WO 0068380-A 48 16-NOV-2000;
Incyte Genomics, Inc. (US)
Incyte Genomics, Inc. (US)
Incyte Gall
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Pred. No. 2.9e-117;
0; Mismatches 64;
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/db_xref="taxon:9606"
/note="Incyte ID No: 2850987CB1"
643 c 680 g 929 t
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                                                                               1835 CATTATAAATGGTGTACAGAACTCCATGAA 1864
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KEYWORDS
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Catarrhini, Hominidae, Homo.
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Pred. No. 2.8e-117
0; Mismatches 64
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Patent: WO 0112659-A 414 22-FEB-2001;
German Human Genome Project (DE)
Location/Qualifiers
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Sequence 414 from Patent W00112659.
AX086462
AX086462.1 GI:13275974
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1 (bases 1 to 3333)
Wiemann, S.
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Eukaryota; Metazoa;
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QGLSGSILSILMGASAIITGIMGTVAFTWLRRKCGLVRTGLISGLAQLSCLILCVISVE
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PIIISVSLLFACVIAARIGLWSFDLTVTQLLQBRVIESBRGIINGVQNSNNYLLDDLHF
PINIIAPNPEAFGLVLISVSFVAMGHIMYFRFAQNTLGNKLFACGFDAKEVRKENQA
NTSVV
                                                                                                                                           A.thaliana T19C21.5"
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DB10B; sites NotI + Sall/MluI"
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315. .2030
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Pred. No. 2.8e-117;
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/note="strong similarity to
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Martinsried (18-JAN-2000) MIPS, Am Klopferspitz 18a, D-82152
Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE2): Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY: Emmil: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/CDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSMB01908 3333 bp mRNA linear PRI 10-MAR-2001
HOMO Sapiens MRNA; cDNA DKFZp586J0624 (from clone DKFZp586J0624);
complete cds.
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Wiemann, S., Weil, B., Wellenreuther, R., Gassenhuber, J., Glassl, S., Misnorge, W., Boecher, M., Balceker, H., Bauersachs, S., Blum, H., Lauber, J., Dusterhoeft, A., Beyer, A., Kochrer, K., Strack, N. Mewes, H.W., Ottenwaelder, B., Obermaier, B., Tampe, J., Heubner, D., Mambutt, R., Korn, B., Klein, M. and Poustka, A.

Toward a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
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/db_xref="taxon:9606"
/map=="939.9 cR from top of Chr2 linkage group"
/clone="DKF2p58650624"
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VLCGTILAMYFLHELLLYRYHGWYLTSCYILLITIANIANLASTATATIORDWIN
VVAGEDRSKLANMNATIRRIDOLTNILAPMAVGQIMTPGSPVIGGGFISGWNIVSMCY
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QGLGGSILGSLAMGAAITGIMGTVAFTWLRRKCGIVRTGI.ISGLAQU.SCLILCVISVY
MPGSPLDLSVSPFEDIRSRTIGGESTTPTKIPETTTEIYMSNGSNSANIVPFTSPESV
PIISWSLLFAGVIARNIGIMSFDLTYTQULQENVIESERGIINGVQNSMYLLDLLHF
INVILAPNPEAFGLLVLISVSFVAMGHIMYFRFAQNTLGNKLFACGPDAKEVRKENQA
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Kackle,A.T., Marciani,P., Rolfs,A., Brennan,K., Wehr,K., Barrow,D.,
Miret,S., Bomford,A., Peters,T.J., Farzaneh,F., Hediger,M.A.,
Hentze,M.W. and Simpson,R.J.
                                                                                                                                                                                                                                                                                                                                                                                                               A novel duodenal iron-regulated transporter, IREG1, implicated in the basolateral transfer of iron to the circulation Mol. Cell 5 (2), 299-309 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (OZ-FEB-2000) Molecular Medicine, King's College London, Guy's, King's and St. Thomas' Medical School, Rayne Institute 123 Coldharbour Lane, London SES 9NU, UK
                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1724 GICCITIGAITIAACIGIGACACAGTIGCIGCAAGAAAAIGIAATIGAAICIGAAAGAGG 1783
                                                           6035 atctctttttatatattaatgaactaaagtgtctttttgtaatgtaggttcagagaatcc 6094
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/gene="IREG1"
/gene="IREG1"
/note="IREG1"
/gene="IREG1"
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/db_xref="taxon:9606"
/chromosome="2"
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AF231121.1 GI:7264728
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 317)
Abboud, S. and Haile, D.J.
A novel mammalian iron-regulated protein involved in intracellular iron metabolism
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Score 646; DB 9; 1
Pred. No. 5.9e-117;
0; Mismatches 65;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                6035 atctctttttatatattaatgaactaaagtgtctttttgtaatgtaggttcagagaatcc
                  tgtattcatgcctggaagcccctggaacttgtccgtttctccttttgaagatatccgatc
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AVSYFLYELYGHSLLTAVYGLYVAGSYLYLDIIGDWYDKNARLKYAQTSLYVONVS
VICGIILAWYFLKHELLTWYHGWYLSCYLILIITIANIAMLASTAFIIORDWIY
VYAGEDRSKLANWMYTRRIDGLTWILAPANYGQIWTFGSPVIGCGFISGWNIYSMCY
EYVLLWKVYQKTPALAVKAGLKEEETELKQINLHKDTEPKPLEGTHLMGVKDSNIHEL
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QGLGSSILLSILMGAGAITGIMGTVAETWLRRKCGIVRTGIJSGLAQLSCLILCVISVS
MPGSPLDLSVSPFEDIRSRFIQGESITPTRID PETTERDMSNGSNSANIVPFETSPESV
PIISWSLLFAGVIARFIGLMSFDLIVTQLLQENVIESERGIINGVQNSMNYLLDLLHF
INVILLAPNPEAFGLLVLISVSFVAMGHIMYFRFAQNTLGNKLFACGPDAKEVPKENQA
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                                             Assignment of slc11a3 to mouse chromosome 1 band 1B and SLC11A3 to human chromosome 2q32 by in situ hybridization Cytogenet. Cell Genet. 88 (3-4), 328-329 (2000)
                                                                                                                                                          Direct Submission
Submission
Submitted (12-DEC-1999) Medicine, UTHSCSA, 7703 Floyd Curl Drive, San Antonio, Tx 78240, USA
Location/Qualifiers
1. 3317
/organism="Homo sapiens"
/db_xref="taxo:9666"
/chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="SLC11A3 iron transporter"
/protein_id="AAF80986.1"
/db_xref="G1:8895485"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 641.2; DB 9;
Pred. No. 5.1e-116;
0; Mismatches 68;
                                                                                                                                                                                                                                                                                                                        /note="iron response element"
305. 2020
/note="ferroportin 1; ireg1"
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ilarity 90.9%;
Conservative
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71. .110
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Haile, D.
               (bases 1 to 3317)
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Matches 682; Conserv
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barren, B., Linton, L., Nusbaum, C., Lander, F., Boguslavkiy, L., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Codge, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Glode, S., Goyette, M., Grand, Plerrer, N., Hagos, B., Heaford, A., Horton, L., Grand Pierre, N., Hagos, B., Heaford, A., Horton, L., Inley, T., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., Macheters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollvar, T., Norman, C. H., Oliver, J., Peterson, K., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Schauer, S., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Traevers, M., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zalnoun, J., Zimmer, A. and Zody, M., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Submitted (30-SEP-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html 1 (bases 1 to 62947).

Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone CTD-2054E23 Unpublished Web site: http://www-seq.wi.mit.edu

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24316: gap of 25082: contiq	5182: gap of 25926: conti	6026: gap of 26765: conti	6865: gap of 27601: conti	ij	: gap of 303: conti	gap of	gap of	gap of	0 -	32607: C	33442: CO	34289: col	35144: co	5244: gap o 35999: co	6099: gap o 36849: co	6949: 9 37675	7775: gap 38533: c	8633: gap o 39359: co	39459: gap of 40174: contig	0274: gap of 40999: conti	1099: gap o 41848: co	ລັ ັ	2804: gap of 43560: conti	3660: gap 44397: c	4497; gap o 45231; co	46079: c	917: c	47774: C	48600: c	49462: C	50318: c	0418: gap 51153: c	1253: gap 52009: c	of	gap of	4: gap of	54575: gap of
421431	508 518	592 602	67 68	760	845 855	930	013	097	107	190	270	354	439	514	600	685 695	767	853	936 946	40175	1100	184 194	270 280	356 366	4449	533	618	701	787	870	956	041	$\frac{115}{125}$	201	283	364	
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                                                                                                       Length 62947;
54576 55298: contig of 723 bp in length 55299 55398: gap of 100 bp 55398. 5634: contig of 736 bp in length 56135 56234: gap of 100 bp 56967 5706: gap of 100 bp 57825 57924: gap of 100 bp 57925 57924: gap of 100 bp 57925 57924: gap of 100 bp 57925 58681: contig of 757 bp in length
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                                                                                                   Score 637.4; DB 2;
Pred. No. 2.5e-115;
0; Mismatches 101;
                                                                                                     8.5%;
                                                                                                                          Conservative
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Best Local Simi
Matches 660;
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PRI 31-AUG-2001

ARVULUJS HOMO Sapiens CDNA FLJ11176 fis, clone PLACE1007386. AK002038

AK002038.1 GI:7023677

DEFINITION ACCESSION VERSION

RESULT 12

AK002038

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Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mall:genomics@tri.co.jp, Tel:81-438-52-3951, Fas:81-438-52-3952) Mahistry of International Trade and Industry of Japan; construction, S- & 3'-end one pass sequencing and clone sequencing. Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MCVKDSNIHELEHEQEPTCASOWAEPFRTFRDGWVSYYNOPVFL
AGMGLAFLYMTVLGFDCITTGYAYTQGLSGSILSILMGASAITGIMGTVAFTWLRRKC
GLVRTGLISGLAQLSCLILCVISVFMPGSPLDLSVSPFEDIRSRFIGGESITPTKIPE
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 2286)

Nishikawa,T., Ota,T., Hayashi,K., Suqiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sato,H., Suqano,S., Shiratori,A., Sudo,H., Magatsuma,M., Hosoliri,T., Kaku,Y., Kodaira,H., Kondo,H., Suqawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Waracanabe,S., Kimura,K., Murakawi,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T. Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="2 bases segment(ta) is present in AF231121
AC013439.9."
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oligo capping; fis (full insert sequence).
momo sapiens placenta cDNA to mRNA, clone_lib:PLACE1
clone:PLACE1007386.
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/clone_lib="PLACE1"
/note="cloning vector: pME18SFL3"
82. .585
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Pred. No. 1.6e-114;
0; Mismatches 64;
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/protein_id="BAA92049.1"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1007386"
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Location/Qualifiers
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sal Similarity 91.2%;
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1 (bases 1 to 513)
Woessner, J., Tan, F., Marra, M., Kucaba, T., Yandell, M., Martin, J., Marth, G., Bowles, L., Wyller, Bowrss, Y., Steptcoe, M., Thoising, B., Gaisel, S., Allen, M., Oderwood, K., Chappell, J., Person, B., Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R., Wilson, R. Riters, E. Kohn, S., Swaller, T., Behymer, K., Hillier, L., Wilson, R. and Waterston, R.
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Missouri 63108,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          6035 atctctttttatatattaatgaactaaagtgtctttttgtaatgtaggttcagagaatcc 6094
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                                                                                                                                                                                      tgtattcatgcctggaagcccctggacttgtccgtttctccttttgaagatatccgatc
                                                                                                                                                                                                                                                    aaggttcattcaaggagagtcaattacacctaccaagatacctgaaattacaactgaaat
                                                                                                                                                                                                                                                                                                                                5615 gtacgcctacactcagggactgagtggttccatcctcagtatttgatgggagcatcagc
                                                                                                                                                                                                                                                                                    AAGGTTCATTCAAGGAGAGTCAATTACACCTACCAAGATACCTGAAATTACAACTGAA - -
                 276 GTACGCCTACACTCAGGGACTGAGTGCTTCCATCCTCAGTATTTTGATGGGAGCATCAC
                                                              tataactggaataatgggaactgtagcttttacttggctacgtcgaaaatgtggtttggt
                                                                                456 TGTATTCATGCCTGGAAGCCCCTGGACTTGTCCGTTTCTCCTTTTGAAGATATCCGATC
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Homo sapiens full length insert cDNA clone YB21H04.
AF147322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6095 attaataaatgatctgaaatgttccctaaa 6124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATTATAAATGGTGTACAGAACTCCATGAA 783
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http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu
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Department of Genetics
Washington University
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FLI_CDNA.
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2 (bases 1 to 513)
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full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved.

Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PRRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to Caenorhabditis elegans protein AAB94213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .213
/note="similar to Arabidopsis thaliana protein AAC28758
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(AC004683) unknown protein
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/organism="Homo sapiens"
/db_xxef="taxon.9606"
/clone="IMAGE:71863"
/clone=lib="Stratagene_fetal_spleen_(#937205)"
1. .294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 513;
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100.0%; Pred. No. 8.1e-91;
7ative. 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                  The location of this clone is unknown Location/Qualifiers
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L (Dasses I to 17443/)

Alsbrooks S.L., Amaratunge, H.C., Are J.R., Banks, T., Barbaria, J., Barbaria, J., Blanks, D., Buck, J., Barbaria, J., Blanks, D., Buck, J., Barbaria, J., Barbton, J., Blankepk, Brown, E., Brown, E., Brown, D., Bouck, J., Burch, J., Briteva, M., Branton, J., Burch, P., Burkett, C., Branch, T.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chaver, D., Chen, G., Chen, R., Carter, M., Cavazos, S.R., Chacko, J., Chaver, D., Chen, G., Chen, R., Corter, M. Dathorne, S.R., David, R., Carter, D., Edaris, C., Barris, C., Barris, R., David, R., Gao, J., Garler, R., Hale, S., Harris, C., Barris, R., Harris, R., Havlak, P., Hane, S., Harris, C., Barris, R., Harris, R., Havlak, R., Hane, J., Jacobson, B., Jis, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, T., King, L., Korvah, J., Jacobson, B., Jis, Y., Ucher, R., Julie, S., Lui, J., Li, J.,
                            A linear HTG 20-DEC-2001
*** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                        Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap; version 0.990329First call to
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Web site: http://www.hgsc.bcm.tmc.edu/
                                  172437 bp DNA norvegicus clone CH230-145018,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: GFQQ
Center clone name: CH230-145018
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                               172437 bp
                                                                                     ***, 59 unordered pieces.
                                                                                                                                                   AC096437.3 GI:17947216
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
OVEE: This is a "working draft' sequence. It currently
consists of 59 contigs. The true order of the pieces
is not known and their order in this sequence record is
Consensus quality: 151836 bases at least Q30 Consensus quality: 158483 bases at least Q20 Estimated insert size: 150873; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarcos-fp estimation Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
                                                                  NOTE: Estimated insert size may differ from sequence length
                                                                                                                                             as soon as it is available and the accession number will be preserved.
                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                             13693: contig of 13693 bp in length
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Yeh, K.-Y., Yeh, M. and Glass, J.
Yeh, K.-Y., Yeh, M.
Submitted (23-JUN-2001) Department of Medicine and Feist-Weiller
Cancer Center, Louisiana State University Health Sciences Center,
1501 Kings Highway, Shreveport, LA 71130, USA
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mRNA, complete cds
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Yeh, W. Yeh, M. and Glass, J.
ron induces ferroportin 1 (FPT1) clustering rat intestinal epithelial cells
Unpublished
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1. 1949
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Rattus norvegicus
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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AUTHORS
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/transl_except= (pos:629..631,aa:Xaa)
/transl_except= (pos:1535..1537,aa:Xaa)
/note= "Xaa= unknown"
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AAL12850
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AAH69131
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               GenCore version 4.5
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99WO-US01404

21-JAN-1999;

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DNA encoding Human breast

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                                                                                                                                                                                                                                                                              The present sequence encodes a human secreted protein. Human secreted activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, haemacopolesis regulating activity, tissue growth activity, activity, chemicially include nativity, chemically activity, chemically include activity, chemically activity, receptor/lighand activity, and thromoblytic activity, receptor/lighand activity, and tumour activity, and tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful
                                                                                                                                                                                                 polynucleotides encoding secreted human proteins derived from fetal brain potentially used as immunostimulators
                                                                                Collins-Racie LA, Fechtel K;
MCCOy JM, Merberg D, Steininger RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1861 BP; 467 A; 402 C; 438 G; 552 T; 2 other;
                                                                                                                                                                                                                                             Claim 15; Page 114-115; 139pp; English.
99US-0235609.
                                                 (GEMY ) GENETICS INST INC
                                                                                , Clark HF,
Lavallie ER,
                                                                                                                                                 WPI; 1999-458682/38
                                                                                                           Wong GG;
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                                                                                Agostino MJ,
20-JAN-1999;
22-JAN-1998;
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Treacy M,
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                                                                                        5435 ctctaacatccatgagcttgaacatgagcaagagcctacttgtgcctcccagatggctga 5494
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  DB 20; Length 1861;
                         64; Indels
8.6%; Score 647.6; DB 20
91.5%; Pred. No. 1.1e-108;
tive 0; Mismatches 64;
             Best Local Similarity 91.5
Matches 686; Conservative
  Query Match
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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; ss; antiinflammatory; immunosuppressive; nootropic; neuroprotective: antiarthritic; antimicrobial; vulnerary; cytostatic; antidabetic; virucide; antinfertulity; anticonvulsant; vasotropic; antiparkinsonian; immunostimulant; dermatological; antirheumatic; antitumor; antiulcer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; araftrversus-host disease; myeloid deficiency; wound healing; ulcer; periodontal disease; myeloid deficiency; wound healing; ulcer; periodontal disease; Huntingon's disease; infection; cardiac disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
gtcctttgatttaactgtgacacagttgctgcaagaaaatgtaattgaatctgaaagagg 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke)
                                                                                                                                           6035 atctctttttatataatgaactaaagtgtctttttgtaatgtaggttcagagaatcc
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Wong GG;
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J, Steininger RJ, Spaulding V,
Merberg D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA encoding a secreted protein ew150_1.
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04-DEC-2000; 2000US-0729674.
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Freacy M, Agostino M
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P-PSDB; AAU39053.
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Clark H,
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various immune deficiencies and disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis, systemic luque erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GVHD), in the induction of tumour immunity, in the treatment of burns, incisions and ulcers; as well as in treatment of burns, incisions and ulcers; as well as in treatment of purns, incisions and ulcers; as well as in treatment of purns, incisions and ulcers; as well as in treatment of purns, incisions and ulcers; as well as in treatment of purns, incisions and streatment of standards and stream and system, Alzhehmer's, Parkinson's disease, Huntington's disease, amylotrophic lateral sclerosis, and Shy-Drager syndrome, infections, infarction of cardiac and central nervous system vessel e.g. stroke, sepsis, inflammatory bowel disease, ulcers, bone regeneration. The protein, having activin- or inhibin-related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in proteins and nucleic acids are also useful as food supplements. The proteins and nucleic acids are also useful as food supplements. The present sequence encodes a secreted protein of the invention.
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91.5%; Pred. No. 1.1e-108;
iive 0; Mismatches 64;
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Best Local Similarity 91.5'
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Human; clone bd306-7; clone yb8-1; ArCC number 98599; gene therapy; limmune disorder; bacterial infection; fungal infection; cancer; tumour; autoimmune disorder; systemic luques erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; activin; haemophilia; cardiac infarction; stroke; sepsis; arthritis; vulnerary; ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; crohn's disease; chemotactic; neuroprotective; haemostatic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New secreted proteins and encoding polynucleotides, useful in gene therapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis, stroke or inflammations -
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                      1495 cattataaatggtgtacagaactccatgaa 1524
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Treacy M, Agostino MJ,
Clark H, Fechtel K;
6095 attaataaatgatctgaaatgttccctaaa
                                                                                                                                                       Human polynucleotide SEQ ID NO 129.
                                                                                ABA90940 standard; cDNA; 1861 BP
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LAVALLIE E R.
COLLINS-RACIE L
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STEININGER R J
SPAULDING V.
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22-JAN-1998;
30-JAN-1998;
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07-JAN-1998;
08-JAN-1998;
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30-MAR-2000;
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20-DEC-1997
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Wong GG,
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The invention relates to isolated polynucleotides (ABA90876-ABA90968 and ABA90980) and encoded proteins (ABB55698-ABB55800), especially controlled to the control of (ABA90885) and SEQ ID NO 10 (ABB55707) contained in proteins SEQ ID NO 12 (ABB55698) and SEQ ID NO 20 (ABB55707) contained in clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 care deposited with the American Type Culture Collection (ATCO) with accession number 98599. The polynucleotides and encoded polypeptides have cytostatic, anti-inflammatory, immunomodulator, vulnerary, curoffective, activity, inhibin, chemotactic, haemostatic, thrombolytic and anti-inflammatory activity and acting as cytokine modulators, haematopoiesis regulators, tissue growth modulators and/or cadherin cuppreprides and polynucleotides are useful in gene therapies, particularly for preventing, treating or ameliorating any of the following diseases: immune deficiency and disorders; e.g. bacterial corruptations of graft-versus-host disease; myeloid or lymphoid cell deficiencies; wound, burns, incisions and ulcers, osteoporosis or corruptaties, central and peripheral nervous system diseases and courtricitis; central and peripheral nervous system diseases and courtricitis; central and peripheral nervous system diseases and courtricitis; central and peripheral nervous system disease, amyotrophic lateral solecois or Shy-Drager syndrome, consistence inflammatory response syndrome, ischaemia-reperfusion consistence consistence inflammatory response syndrome, ischaemia-reperfusion consistence consistence in the consistence of consistence of consistence in the consistence of consistence in the consistence in the consistence of consistence in the consistence in the
Page 269-270; 349pp; English.
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Sequence 1861 BP; 467 A; 402 C; 438 G; 552 T; 2 other;

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                        Indels
   DB 24;
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  Score 647.6; DB 24
Pred. No. 1.1e-108
0; Mismatches 64
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Ouery Match 8.6
Best Local Similarity 91.5
Matches 686; Conservative
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The invention relates to novel genes (AAH68727-AAH73383) associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the
                                                                                                                                                                                                                                                                                                                                                                       Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
gtcctttgatttaactgtgacacagttgctgcaagaaaatgtaattgaatctgaaagagg 1494
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                                                        6035 atctctttttatatattaatgaactaaagtgtctttttgtaatgtaggttcagagaatcc
                                          gcccataatctctgtcagtctgctgtttgcaggcgtcattgctgctagaatcggtaagaa
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Pred. No. 1.1e-108;
0; Mismatches 64;
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                                                                                                                                                                                                                                                                                                                                           Human cervical cancer marker
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99US-0171350.
2000US-0189315.
2000US-0203791.
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Best Local Similarity 91.5%;
Matches 686; Conservative
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2000US-0220114
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09-JUN-2000;
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21-DEC-1999;
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                                                                  gtacgcctacactcagggactgagtggttccatcctcagtattttgatgggagcatcagc
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The present invention provides the protein and coding sequences for 25 novel extracellular matrix and adhesion-associated proteins (EXMADS). These are designated EXMAD-1, EXMAD-2, EXMAD-1, EXMAD-1, EXMAD-5, EXMAD-1, EXMAD-2, EXMAD-3, EXMAD-2, EXMAD-2, EXMAD-2, EXMAD-3, EXMAD-2, EXMAD-2, EXMAD-3, EXMAD-1, EXM
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                                                                                                                                                                                                       MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polynucleotide encoding extracellular matrix or adhesion-associated protein (EXMAD) useful for diagnosing, tre preventing disorders associated with expression of EXMAD such
                                                                                                                                                                                                           Baughn
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Pred. No. 1.2e
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Best Local Similarity 91.5%;
Matches 686; Conservative 0
99US-0133643.
                                                                                                                        GENOMICS INC
                                                                                                                                                                                                       Hillman JL,
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11-MAY-1999;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
1630 atacatgtctaatgggtctaattctgctaatattgtcccggagacaagtcctgaatctgt 1689
                                                                                                              1750 gtcctttgatttaactgtgacacagttgctgcaagaaaatgtaattgaatctgaaagagg 1809
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                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance: peripheral nervous system; cns; paripheral nervous system; cns; Alzheimer's; Parkinson's disease; Muntington's disease; Maemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang
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                            6035 atctctttttatatattaatgaactaaagtgtctttttgtaatgtaggttcagagaatcc
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Zhang J;
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Yang Y,
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                                                                                                                                                         such as central nervous system injuries
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                                                                                                                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 4065.
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2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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Zhou P,
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14-SEP-2000;
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09-JUL-2000;
19-JUL-2000;
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           and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
 Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
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                                                                                                                      Length 3328;
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                                               not form part of
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                                                                                  Sequence 3328 BP; 1032 A; 699 C; 670 G; 927 T; 0 other;
                                                                                                                      Score 647.6; DB 22;
Pred. No. 1.2e-108;
                                                                                                                                             64;
                                             Note: The sequence data for this patent did
                                                                                                                                            0; Mismatches
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                                                                                                                     Query Match 8.6%;
Best Local Similarity 91.5%;
Matches 686; Conservative
                                   disorders
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                  gccttccgtaccttccgagatggatgggtctcctactacaaccagcctgtgtttctggc
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.6%; Score 647.6; DB 22; Length 3454;
llarity 91.5%; Pred. No. 1.2e-108;
Conservative 0; Mismatches 64; Indels 0;
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Yang Y,
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Xu C, Xue AJ,
R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          such as central nervous system injuries
                              Human polynucleotide SEQ ID NO 493.
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Goodrich R,
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2000us-0598042.
2000us-0620312.
2000us-0653450.
2000us-0653450.
2000us-0693036.
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Wang Z, Wehrman T,
Zhou P, Goodrich
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                                                                                                                                leukaemia; ss.
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14-SEP-2000;
19-OCT-2000;
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Matches 686;
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Matches 713;
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                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical insering of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cappanestic for gene mapping, identification of mutations are responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and .
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                                                   New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 647.4; DB 23;
Pred. No. 1.3e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic coding sequences of the invention.
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                                                                                                                                       Claim 1; SEQ ID No 20253; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.6%;
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Best Local Similarity 97.6
Matches 657; Conservative
2001-639362/73
                    P-PSDB; ABG20262
                                                                                                        biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                geceataatetetgteagtetgetgtttgeaggegteattgetgetagaateggtaagaa
                                                                          atacatgtctaatgggtctaattctgctaatattgtcccggagacaagtcctgaatctgt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human breast cancer expressed polynucleotide 15579.
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Pred. No. 1.2e-106;
0; Mismatches 20;
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15-MAY-2000;
09-JUN-2000;
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02-MAY-2000; 2000JP-0183767.
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                                                                                                                                                                                                                                                                                  Human; primer; detection; diagnosis; antisense therapy; gene therapy;
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                                          gttetttgecaaagtegtegttgtagtetttttgeceaaggetgttgtgtttttagaggt
                                                                              tagcagccgcagaagagccagcggggtcgcctagtgtcatgaccagggcgggagatcaca
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                     aattcagggtgtgggaaaaggggtttgcacacaggcacggatggagtagattgggcagtt
GGGAGACCTGGTGAGCCTCCCAAACGGCTTCCATAGGGCTTGCCCTTTCAAATTTAAGTT
              GTTCTTTGCCAAAGTGGTCGTTGTAGTCTTTTTGCCCAGGGCTGTTGTGTTTTAAAGGT
                                                                      gctatctccagttccttgcactcctgttaacaagcacctcagcgagagcagcagcga
                                                                                                                TAGCAGCCGCAGAAGAGCCAGCGGGGTCGCCTAGTGTCATGACCAGGGCGGGAGATCACA
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                                                                                                                                                                                                                                                                                                                                         Human cDNA sequence SEQ ID NO:12958.
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27-AUG-1999;
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The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set
comptises: (a) an oligo-dT primer and an oligouncleotide complementary
to the complementary strand of a polypuncleotide which complementary
to the sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprises a 3'-end sequence of the sequence
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                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID 12958; 2537pp + CD ROM; English.
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                                                                                                       Nagai K,
                                                                Hayashi K,
A, Nagai K
                                                                                                              Wakamatsu
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  Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                     gcccataatctctgtcagtctgctgtttgcaggcgtcattgctgctagaatcggtaagaa 6034
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694 gtcctttgatttaactgtgacacagttgctgcaagaaaatgtaattgaatctgaaagagg 753
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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                               tgcccataatctctgtcagtctgctgtttgcaggcgtcattgctgctagaatcggtaaga
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                                                                   ctgtattcatgcctggaagcccctggacttgtccgtttctccttttgaagatatccgat
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Otsuki
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A, Nagai K,
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAX-2000; 2000JP-0183767.
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The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for described uses).
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Freng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS,
Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human genes and the secreted polypeptide(s) they encoder second for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 375-376; 721pp; English.
97US-0056908.
97US-0056909.
97US-0056910.
97US-0056911.
97US-0057650.
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97US-0057761.
97US-0058785.
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Matches 685; Conservative
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22-AUG-1997;
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05-SEP-1997
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<u>ب</u>

Yamamoto ÷

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(first entry)

07-DEC-2001

AAL21721;

Human; breast cancer; cell marker; cytostatic;

10-JAN-2001; 2001WO-US00798

WO200151628-A2.

19-JUL-2001

2000US-0176077

14-JAN-2000;

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                 of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence. Where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13633 to AAH13632 represent human cDNA sequences; AAB92446 to AAH13632 represent human amino acid sequences: and AAH13629 to AAH13632
                                                                                                                                                                                                                                                              represent oligonucleotides, all of which are used in the exemplification
oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complements to the
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                                                                                                                                                                                                                                                                                                                                                               8.2%; Score 612.4; DB 22; Length 683; 98.3%; Pred. No. 2.3e-102; 1ve 0; Mismatches 9; Indels 2;
                                                                                                                                                                                                                                                                                                               Sequence 683 BP; 172 A; 157 C; 154 G; 197 T; 3 other;
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Matches 628; Conserv
                                                                                                                                                                                                                                                                                                                                                                  Query Match
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The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity.
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20000S-0192099.
20000S-0193480.
20000S-0205230.
20000S-021315.
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24-MAR-2000;
29-MAR-2000;
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09-JUN-2000;
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RESULT 13 AAL21721/C ID AAL21721 standard; cDNA; 774

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23. MAY - 1997
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The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAVS9511-V59812; amino acid sequences AAN74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypetides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ides, based on which tissues they are most highly expressed in
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Olsen HS, Rosen CA;
L, Zeng Z;
                                                                                                                                                                                                                                                                                    New isolated human genes and the secreted polypeptide(s) they encoc - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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Le AM, Fischer CL,
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Kyaw H, Lafleur DW, Li Y, M
Puhan SM, Shi Y, Soppet DR,
97US-0056892.
97US-0056893.
97US-0056894.
97US-0056908.
97US-0056909.
97US-0056910.
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                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                  WPI; 1998-506364/43.
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2000US-0205230.
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25-JUL-2000;
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polypeptides are also useful for isolating compounds with cytostatic activity.
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APPLICANT: Hendrickson, Eric
TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and
TITLE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity
FILE REFERENCE: B087777017/HK
CURRENT APPLICATION NUMBER: US/09/173,914
CURRENT FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: 60/064,557
EARLIER FILING DATE: 1997-10-17
SOFTWARE: FASISEQ for Windows Version 3.0
SOFTWARE: FASISEQ for Windows Version 3.0
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Pred. No. 1.1e-51;
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US - 09 - 128 - 155 - 17

US - 09 - 724 - 394A - 21

US - 08 - 724 - 394A - 22

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Matches 286; Conservative
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/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-128-133-105-633-105-633-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-133-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638-105-638
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                          nucleic search, using sw model
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US-08-742-185-102
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            Sequence 105, Application US/08687080
Patent No. 5965427
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: 350 Cambridge & Associates
STREET: 350 Cambridge Avenue, Suite 250
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                                                                                                                                                                                          COMPUTER READABLE FORM:

CIP: 94306

COMPUTER READABLE FORM:

MEDIDIM TYPE: Floppy disk

COMPUTER: IM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/687,080

FILING DATE: 17-JUL-1996

CLASSIFICATION: 435

PRICR APPLICATION NUMBER: US 08/592,126

FILING DATE: 26-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615

REPERBONE: (415) 324-0960

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:

LENGTH: 13158 base pairs

TYPE: NUCLEIC ACUBE
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Best Local Similarity 80.6
Matches 307; Conservative
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                                                                                                                                                    CITY: Palo Alto
STATE: CA
                                                                                                                                                                                       USA
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ORIGINAL SOURCE:
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US-08-687-080-105
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GENERAL INFORMATION:
GURRENT APPLICATION NUMBER:
GURRENT FILING DATE:
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SOFTWARE:
FRASEEQ for Windows Version 4.0
SEQ ID NOS:
SEQ ID NOS
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Patent No. 6020476
GENERAL INFORMATION:
APPLICANT: Page, David C.
APPLICANT: Reijo, Renee
APPLICANT: Sacena, Richa
APPLICANT: Sacena, Richa
APPLICANT: Hawkins, Trevor
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CTHER INFORMATION: n = A,T,C or
US-09-797-906-3
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Sequence 5, Application US/08629939 Patent No. 5645995
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APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCE: 102
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 40328;
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                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/690,734
FILING DATE: 31-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/310,429
FILING DATE: 21-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.5%; Score 260.2; DB 3; Best Local Similarity 84.6%; Pred. No. 1e-49; Matches 292; Conservative 0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Grandan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 34,227
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 861-6240
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 4028 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                       ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) US-08-742-185-102
                                                                                                      STATE: Massachusetts
COUNTRY: US
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US-08-629-939-5

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4995 tgcccgcctcggcctcccaaagtgctgggattacaggtgtgagccaccgtgcctggccaa 5054
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                   Dirk G.
METHODS FOR DIAGNOSING AN INCREASED
RISK OF BREAST OR OVARIAN CANCER
              APPLICANT: Kieback, Dirk G.
TITLE OF INVENTION: METHODS FOR DIAGNOSING AN INCREATITLE OF INVENTION: RISK OF BREAST OR OVARIAN CANCER NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT SPELICATION DATE: 12-APRIL-1996
FLING DATE: 12-APRIL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6612
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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89.4%; Pred. No. 2e-50;
tive 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-08-759-873-5
; Sequence 5, Application US/08759873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 89.43
Matches 279; Conservative
                                                                                                                                                                               CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5055 tacgetgtgttt 5066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 20037
GENERAL INFORMATION:
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GENERAL INFORMATION:
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                           Dirk G.
METHODS FOR DIAGNOSING AN INCREASED RISK
OF BREAST OR OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 259.2; DB 1; Length 320;
Pred. No. 2e-50;
0; Mismatches 33; Indels 0
                                                                                                                                                                                                        CAPPUTER TOUGH TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: END PC compatible
COMPUTER: END PC compatible
CORERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DARPS:
APPLICATION NUMBER: US/08/759,873
FILING DATE: 12-APRIL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KIT, GORDO
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6612
TELEPHONE: (202) 293-7060
TELEPHONE: (202) 293-7060
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: single
                                                                                                            ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W., Suite 800 STATE: D.C. COUNTRY: U.S.A.
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89.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.5
Best Local Similarity 89.4
Matches 279; Conservative
          GENERAL INFORMATION:
APPLICANT: Kieback, Dirk
TITLE OF INVENTION: WET
TITLE OF INVENTION: OF E
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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; Sequence 101, Application US/08742185 ; Patent No. 6020476

US-08-742-185-101

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6648 CAGCTAATTTTTGTGTTTTTAGTAGAGATGGGGTTTCATCGTGTTAGCCAGGATGGTCT 6707
                                                                                                                   TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgagocaccgtgcctggccaatacgctgtgtttttttagacaattttaatattt 5088
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Pred. No. 2e-49;
0; Mismatches 60; Indels 0
                                                                                                                                                                                                                                                                                                                         COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION: 435
FILING DATE: 31-0CT-1996
FILING DATE: 31-JUL-1996
FILING DATE: 31-JUL-1996
FILING DATE: 22-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: Granahan, Patiticia
REGISTRATION NUMBER: WHI94-07A2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: WHI94-07A2
TELECOMMUNICATION NUMBER: WHI94-07A2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NOTION: 101:
                                                                                                                                                                                     E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic)
US-08-742-185-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 83.1%;
Matches 295; Conservative (
                      APPLICANT: Reijo, Renee
APPLICANT: Saxena, Richa
APPLICANT: Hawkins,Trevor
APPLICANT: Reeve, Mary Pat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 43795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
: Page, David C.
: Reijo, Renee
                                                                                                                                                                                                               STREET: Two Militia I
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4914
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3226 GGGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCC 3167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3286 TITITITITITITITITIGEGAGGAGTCTTGCTCTGTCGCCCAGGCTGGAGTGCAGGCG 3227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4815 gcgatcttggctcactgcaagctctgcctcctgggttcacgccattctcctgcctcagcc 4874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTY: USA
ZIP: 94111-3834
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILLNG DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                       3.4%; Score 258; DB 2;
91.6%; Pred. No. 7.6e-49;
tive 0; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35,136
ER: 017957-000100
                                                                                                                                                                                                               RESULT 9
US-08-724-394A-20/c
; Sequence 20, Application US/08724394A
; Patent No. 5877237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION UNDBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                       APPLICANT: Feder, John N. APPLICANT: Kronmal, Grego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.4
Best Local Similarity 91.6
Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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6768 TGAGCCACCGTGCCCAGCCAAAAGATTTTTTTTAAGAGAGAATCTTACTATATT 6822
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Pred. No. 8.3e-50;
0; Mismatches 49; Indels 0;
                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Adamou, Julie
APPLICANT: Adamou, Julie
APPLICANT: Rirkpatrick, Robert
APPLICANT: Rosenberg, Martin
TITLE OF INVENTION: HUMAN CARTILEGE GP39-LIKE GENE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,915
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                                                                                                       Sequence 5, Application US/08694915 Patent No. 5811535
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NAME: Han, William T
REGISTRATION NUMBER: 34,344
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 3742 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.4
Best Local Similarity 85.5
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                       STREET: 709 Swedeland
CITY: King of Prussia
STATE: PA
COUNTRY: USA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: CDNA
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; ORIGINAL SOURCE:
US-08-694-915-5
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                                                                RESULT 8
US-08-694-915-5/c
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4755 ttgttttttgttttttgagacagagtctcgctctgttgcccaggctgaagtgcagtggc 4814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Lauer, Peter M.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Pred. No. 7.6e-49;
0; Mismatches 25; Indels
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ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION *536
ATTORNEY/AGENT INFORMATION:
NAMME: FILICA ROMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFOR
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CITY: San Francisco
STATE: CA
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| LOCATION: 1..246240
| OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/08724394A Patent No. 5872237
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TOPOLOGY: not relevant
DLECULE TYPE: CDNA
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91.6%;
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Matches 273; Conservative
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US-08-724-394A-21/c
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gegatettggeteactgeaagetetgeetectgggtteacgeeatteteetgeeteagee 4874
                                            3226 GGGATCTCGCCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCC 3167
                                                                                             teceaagtagetgggattgeaggeatecaceaceacecegetaatttttgtatttt 4934
                                                                                                                          3166 TCCCAAGTAGCTGGGACTACAGGCGCCCGCACTACGCCCGGCTAATTTTGTATTTT 3107
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ZIP: 94111-3834
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: NO
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CITY: San Francisco
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LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
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; Sequence 22, Application US/08724394A
; Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNET/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179:
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-576-0300
TELEPARX: 415-576-0300
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
FRNGTH: 246240 base pairs
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Matches 273; Conservative
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ADDRESSEE: TOWNSEND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: not 1
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MOLECULE TYPE: CDNA
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cgatcttggctcactgcaagctctgcctcctggttcacgccattctcctgcctcagcct
                              8873 GATCTCGGCTCACAGCACCTCCACGTTCACGCCATTCTCCTGCCTCAGCCT
                                                             cccaagtagctgggattgcaggcatccaccacaccggctaattttttgtattttta
                                                                               4996 gecegecteggecteceaaagtgetgggattacaggtgtgagecacegtgeetggecaat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 14796;
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ilarity 88.6%; Pred. No. 2.9e-49;
Conservative 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09630706
Patent No. 6277640
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lax M. Cowsert
TILE OF INVENTION: ANTISENSE MODULATION OF HEE
FILE REFERENCE: RTS-0053
CURRENT APPLICATION NUMBER: US/09/630,706
CURRENT FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 94
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (5158)...(5275)
NAME/KEY: CDS
LOCATION: (11955)...(12044)
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NAME/KEY: CDS
LOCATION: (2811)...(2921)
NAME/KEY: CDS
LOCATION: (3174)...(3283)
NAME/KEY: CDS
LOCATION: (5158)...(5275)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity
Matches 279; Conserv
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US-09-630-706-10/c
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                             3286 TITITITITITITITITITIGAGACGGAGTCTTGCTCTGTCGCCCAGGCTGGAGTGCAGTGGC 3227
                                                                                                                        4875 tcccaagtagctgggattgcaggcatccaccaccaccccggctaatttttgtatttt 4934
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US-08-975-080-35/c
US-08-975-080-35/c
); Sequence 35, Application US/08975080
); Patent No. 6245523
); GENERAL INFORMATION:
| APPLICANT: Altieri, Dario C.
| TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
| TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
| TITLE OF INVENTION: 35
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Pred. No. 2.9e-49;
0; Mismatches 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/975,080 FILING DATE: 20-NOV-1997 PRIOR APPLICATION NUMBER: US 60/031,435 FILING DATE: 20-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-467-7176 INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) US-08-975-080-35
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Best Local Similarity 88.6%;
Matches 279; Conservative (
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LENGTH: 14796 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CHARLEANT: C. FIRTH Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Eric E. Swayze
APPLICANT: Lex M. Cowsert
FILE REFERENCE: ISPH-0439
CURRENT APPLICATION NUMBER: US/09/496,694B
CURRENT APPLICATION NUMBER: 09/286,407
PRIOR APPLICATION NUMBER: 09/286,407
PRIOR PILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 09/163,162
PRIOR PILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 249
SEQ ID NO 3
TENCTH: 14796
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Pred. No. 2.9e-49;
0; Mismatches 36;
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; Sequence 128, Application US/09385982
; Patent No. 6262334
                                                                         Sequence 3, Application US/09496694B
Patent No. 6335194
GENERAL INFORMATION:
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Best Local Similarity 88.6
Matches 279; Conservative
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5056 acgctgtgtttttt
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-09-496-694B-3/C
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LOCATION: (28)
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            GENES AND GENE EXPRESSION
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TITLE OF INVENTION: NOVEL HUMAN GENES AND GE TITLE OF INVENTION: NOVEL HUMAN GENES AND GE TITLE OF INVENTION: NOVEL HUMAN GENES AND GE TITLE OF INVENTION: PRODUCTS: II
FILL REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-30
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FESSESEQ for Windows Version 3.0
SEQ ID NO 128
LENGTH: 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: July 24, 2002, 00:05:20 Job time: 26245 sec
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                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(588)
; OTHER INFORMATION: n = A,T,C or
US-09-385-982-128
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453 6.0 3071 11 AK008700 450.8 6.0 932 10 BG286556 449.4 6.0 451 9 AA563938 443.8 5.9 586 10 BG689712	23 432.4 5.8 56 10 BG942981	C 24 431.8 5.8 456 9 A1248642 A1248642 Gn77d05.x C 25 425.2 5.7 431 9 AN359532 AN359532 Lp32all.x C 26 425 5.7 433 9 A133945 A1539532 Lp32all.x 27 421.6 5.6 726 9 A1338245 A138245 A138245	29 418.6 5.6 665 9 BB623179 30 418 5.6 443 9 AI127313 31 414.2 5.5 434 9 AI874113	410.6 3.5 3.95 10 W2340.1 406.4 5.4 439 9 AL599331 404 5.4 987 9 AL551987	35 403.4 5.4 431 9 AA4.2611/ 36 390.4 5.2 1054 10 BF788989 37 387 5 5 401 9 BT973310	307.5 5.2 401 9 A13/5/210 387 5.2 425 9 AA2/5/21 383 4 5 1 75 10 B115/6/5/7	375 5.0 759 9 AL572951 363.4 4.8 434 10 D82422	349 4.7 349 9 348 4.6 515 10 347 4.6 563 9 341.2 4.6 603 10	ALIGNMENTS	RESULT 1		ACCESSION BE069938 VERSION BE069938.1 GI:8409134 KEYWORDS EST.	SM	REFERENCE 1 (Dases 1 to 624) AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,	Angari, A. Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and	TITLE Shoton sequencing of the human transcriptome with ORF expressed	JOURNAL Proc. Lays JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) MEDLINE 20202663		Brazil Tel: +55-11-2704922 Fax: +55-11-2707001	Email: asimpson@ludwig.org.br This sequence aderived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL	(http://www.ludwig.org.br/scripts/getntmiz.pl?tl=&t2=RC4-BT0311-250 200-014-b06&f3=2000-02-25&t4-1) Seq_primer: puc 18_forward		source 1624 /organism="Homo sapiens"
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: July 23, 2002, 16:43:00 ; Search time 7392.1 Seconds (without alignments) 13686.662 Million cell updates/sec	Title: US-09-715-927-7 Perfect score: 7496 Sequence: 1 agctggctcagggcgtccgcgttgaggcatggaaaaaaa 7496	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 13736207 seqs, 6748477542 residues	Total number of hits satisfying chosen parameters: 27472414	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	⊢		6: em_estpl:* 7: em_estro:*				Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID Description	614.2 8.2 624 9 BE069938 612.4 8.2 683 9 AU13785.2 603.8 8.1 875 10 BG536539	8.0 913 9 7.7 911 10 7.2 631 10	519.2 6.9 810 9 AUL33566 519.2 6.9 896 9 AL550578 505.6 6.7 771 9 AUL34630	200.0 0.7 018 9 AMPOSASA 496.2 6.6 732 10 BISS465 494.4 6.6 859 9 AL577308	13 491.0 6.0 5/2 12 AQ/28/06 14 488 6.5 727 10 BG618204 15 482.2 6.4 731 9 AV704855 15 73 73 73 73 73 73 73 73 73 73 73 73 73	470 6.3 513 10 BI002788 455.6 6.1 958 9 AL545521

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FEATURES
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                       /note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue markA and cDNA amplification were performed under low stringency configures.
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/db_xref="taxon:9606"
/clone_lib="BT0311"
/dev_stage="Adult"
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KEYWORDS
SOURCE
ORGANISM
                                                                                         BASE COUNT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 683)
                                                                                                                    Unpublished (2000)

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Email: genomics@hri.co.jp

Fix: 81-438-52-367

Email: genomics@hri.co.jp

Fix: 81-438-52-367

Email: genomics@hri.co.jp

Winology, Institute; ObNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and
                                      Saito,K., Kawai,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gccttccgtaccttccgagatggatgggtctcctactacaaccagcctgtttctggc 5554
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|TTACACAAAGATACTGAGCCAAAACCCCTGGAGGAACTCATCTAATGGGTGTGAAAGA 95
                                                    Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,1
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S.
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Pred. No. 2.1e-74;
0; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            : pME18SFL3"
154 g 197
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98.38;
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Matches 628; Conservative
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181 TCACCACAGGGTACGCCTACACTCAGGGACTGAGTGGTTCCATCCTCAGTATTTTGATGG 240
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
DNA Sequence stop: 739.
Plate: LLCMISOS row: 1 column: 11
High quality sequence stop: 739.
Location/Qualifiers

J. .875
Location/Qualifiers

J. .875
Location/Qualifiers

J. .875
Location/Qualifiers

J. .875
Location-Lib="NHUM GC-77"

Ab_Lxref="taxon:9606"

Clone="ImAGE:#489562"

Clone="ImAGE:#4895
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 875)
1 (hases 1 to 875)
1 National http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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574 ATACATGTCTAATGGGTCTAATTCTGCTAATATTGTCCCGGAGACAANTCCTGAATCTGT 633
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                                            Ouery Match 8.1%; Score 603.8; DB 10;
Best Local Similarity 98.1%; Pred. No. 2.9e-73;
Matches 611; Conservative 0; Mismatches 12;
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                                                                                                                                                                                                                                                                            mRNA sequence.
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/db_xref="taxon:9606"
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/tissue_type="placenta"
/fote="Vector: pCWVSPORT 6; Site_1: Not1; lst strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and Cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies.
a division of Invitrogen 9800 Medical Center Drive Rockvilla, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"

http://fulllength.invitrogen.com"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                  Genoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - France
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
_Location/Qualifiers
                                                                                   5785 gtgtgatctctgtattcatgcctggaagccccctggacttgtccgtttctccttttgaag
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Li,W. B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Local Best Loca Matches

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/clone="InAGE-4271059"
/clone="InAGE-4271059"
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and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
c, or G and N = A, C, G, or T). Average insert size
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enritched for full-length clones and was constructed by Clontech Laboratories (Palo
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Best Local Similarity 97.2%; Pred. No. 5.7e-70;
Matches 632; Conservative 0; Mismatches 14
     Plate: LLCM1082 row: n column:
High quality sequence stop: 632.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 911)
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Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
                    Gaps
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                  Indels
97.6%; Pred. No. 1.5e-72; ive 2; Mismatches 12;
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Contact: Robert Strausberg, Ph.D.
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BF574374.1 GI:11648086
                  616; Conservative
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LOCUS DEFINITION

BF574374

RESULT

ACCESSION VERSION KEYWORDS

ORGANISM

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

5614

Gaps

4

14; Indels

Length 911;

DB 10;

5914

554

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810 bp mRNA linear EST 24-OCT-2000 OVARC1 Homo sapiens cDNA clone OVARC1000166 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genomicseri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Hellx Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
151 81-438-52-3951
Fax: 81-438-52-3952
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/note="Vector: pME18SFL3"
150 c 152 g 265 t 3
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Pred. No. 1e-61;
0; Mismatches
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/clone_lib="OVARC1"
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HRI human cDNA project
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Best Local Similarity 99.4%;
Matches 521; Conservative 0
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Contact: Takao Isogai
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                                EST 06-NOV-2001
                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 631)

Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
                                                                                                                                                                                                                                                                                                                                      GlaxosmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Fax: 610-270-7559
Email: sanjay_kumar-10gsk.com
Seq primer: T7.
Location/Qualifiers
                                            HNC26-1-D1.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.2%; Score 543.4; DB 10; Length 631; Similarity 99.6%; Pred. No. 5.6e-65; 14; Conservative 0; Mismatches 2; Indels 0;
                                linear
                              mRNA
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/tissue_type="placenta"
/tissue_type="placenta"
/tissue_type="placenta"
/tissue_type="placenta"
/note="weetor: pCMVSDORT 6; Site_1: NotI; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com"

http://fullength.invitrogen.com"
10 thers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Manmalla; Euthberia; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 896).
S Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
LU Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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AL550578 LTI_NFL006_PL2 Homo sapiens CDNA clone CSODI058YG22 5
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GATTTCAGTCTCCTTTGTGGCCAATGGGCCACATTATGTATTTCCGATTTGCCCAAAATAC 297
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/db_xref="taxon:9606"
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 771)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                   7272
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171 TCTGCATTTCATCATGGTCATCCTGGCTCCAAATCCTGAAGCTTTTGGCTTGCTCGTATT
                                                                       tctgcatttcatcatggtcatcctggctccaaatcctgaagcttttggcttgctcgtatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai,T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Hellx Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
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/db_xref="Leixon: 9606"
/clone="PLACE1000166"
/clone_lib="PLACE1"
/tissue_type="placenta"
/note="Vector: pME18SFL3"
a 142 c 155 g 243 t
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AU134630.1 GI:10995169
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Ism Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammaliar; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 732)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Optublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbb:-r@mail.ih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLONE distribution: MGC Clone distribution information can be http://image.llnl.gov

Plate: LiAmils70 row: m column: 19

High quality sequence stop: 730.

Location/Qualifiers
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                                                            Score 500.6; DB Pred. No. 4e-59; 0; Mismatches
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BI835465
BI835465.1 GI:15947015
                                                              6.7%;
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                                                              Query Match 6.7
Best Local Similarity 98.3
Matches 506; Conservative
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   146
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BI835465
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DEFINITION
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 BASE COUNT
ORIGIN
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Contact: John Quackenbush
From Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 528
Fax: 301 838 0208
Email: johnq@tigr.org
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 618)
Hegde, P., 01,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., 1.E., Saed-A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
                                                                                                                                        tgaatctgaaagaggcattataaatggtgtacagaactccatgaactatcttcttgatct
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   Length 771;
                               Indels
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGH"
/note="Vector: pBluescriptSKm"
Score 505.6; DB 9;
Pred. No. 7.6e-60;
0; Mismatches 5;
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1. .618
6.7%;
ilarity 98.9%;
Conservative
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 Query Match
Best Local Similarity
Matches 519; Conserv
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AW963336
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Conservative
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AUTHORS
TITLE
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     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE=5226810"
/clone=lib="NHH_MGC_120"
/clone=lib="NHH_MGC_120"
/clone=lib="NHH_MGC_120"
/clone=lib="Sorgen pooled pencreas and spleen; Vector:
pcMv-SPORT6; Site_l: Not1; Site_2: EcoRv (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRv site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    859 bp mRNA linear EST 16-FEB-2001
prime, mRNA sequence.
AL577308
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 859)
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Pred. No. 1.5e-58;
0; Mismatches 3; Indels
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                                                                                        : www.genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctcagtattttgatgggagcatcagctataactggaataatgggaactgtagcttttact
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0
                                                                                                                                                                                                                                                                                                                                                                                                       6.6%; Score 494.4; DB 9; Length 859; 89.1%; Pred. No. 2.5e-58; Live 2; Mismatches 63; Indels 0
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
                                                         Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www
Location/Qualifiers
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/db_xref="taxon:9606"
/dlone="IMAGE:4767414"
/clone="IMAGE:4767414"
/clone="IMAGE:4767414"
/clone="IMAGE:4767414"
/clone="IMAGE:16"
/lab_host="DHIOB (TI phage-resistant)"
/lab_host="DHIOB (TI phage-resistant)"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggocgetcuggcc); Site_2: Sfil (ggocgettatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACATGGCCATGGC-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH, MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG618204 727 bp mRNA linear EST 18-APR-2001 602645928F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4767414 5',
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11 HMC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
      7122
                                                                                                                                                                                                                                               7243 tgatgcaaaagaagttaggaaggaaaatcaagcaaatacatctgttgtttgagacagttt 7302
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      acagaactccatgaactatcttcttgatcttctgcatttcatcatggtcatcctggctcc
                                                                                                                                                                                                                                                                                                                                                                                                         149 TGATGCAAAAGAAGTTAGGAAGGAATATCNAGCNAATACATCTATAGAAAGAGACAGTTT
                                                            329 ACAGAACTCCATGAACTATCTTGATCTTCTTGCATTTCATGATGGTCATGCTGGCTCC
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0; Mismatches
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BG618204.1 GI:13669575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avonue North, Seattle, WA 98109, USA
7e1: (206) 616-3618
Fax: (206) 616-3887
Email: jWallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@tesgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="lplate=1055 col=23 Row=O"
/clone=11b="RPCI-11 Human Male BAC Library"
/sex="male"
/note="vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the BBACe3.6 vector as 15e ECORI sites"

10 c 95 g 10 C 12 others
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                      AQ728706 572 bp DNA linear GSS 15-JUL-HS_5479_Al_H12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1055 Col=23 Row=0, DNA sequence.
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94.5%; Pred. No. 6.9e-58;
Live 0; Mismatches 29;
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Location/Qualifiers
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Seq primer: T7
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 731)

RS Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Gung,Y., Gun,J., Chen,Z., and Han,Z., and Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV704855 ADB Homo sapiens cDNA clone ADBCDB11 5', mRNA sequence. AV704855.1 GI:10722167
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/dev_stage="Adnit"
/lab_host="Solls"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
  7044
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/clone_lib="ADB"
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Pred. No. 1.2e-56;
0; Mismatches 19;
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